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FIGURE 1A

Frame3 L C S L L F G L S L S I T M F E M M P
 Frame2 V M * S F V W S L P * H N D V * D D A I
 Frame1 C Y V V F C L V S P L A * R C L R * C H
 DNA TGTATGTAGTCTTTTGGTCTCTCCCTAGCATAACGATGTTTGAGATGATGCCAT 60
 K hcv16029210 rpt

.....
 Frame3 F I H F C C * A A A E Y C W N P S L F I
 Frame2 H S F L L L S S C R V L L E S Q F I H W
 Frame1 S F I F V A E Q L P S I V G I P V Y S L
 DNA TCATTCATTTTGTGCTGAGCAGCTGCCGAGTATTGTTGGAATCCAGTTTATTCATTG 120
 Y hcv26544776 SNPG98 AL662833

.....
 Frame3 G F C V S S * * T C G F L Q L G F V I N
 Frame2 F L C L Q L I D M W I P P V R V C Y * *
 Frame1 V S V S P V D R H V D S S S * G L L L M
 DNA GTTCTGTGTCTCCAGTTGATAGACATGTGGATTCTCCAGTTAGGGTTTGTATTAAATG 180
 Y hcv26544777 rpt
 | SNPG168 AL662833

.....
 Frame3 E A T I N N C L Q V W T Y I F I S F G *
 Frame2 S H Y K * L L T S V D L H F Y F F W I N
 Frame1 K P L * I T A Y K C G L T F L F L L D K
 DNA AAGCCACTATAAATAACTGCTTACAAGTGTGGACTTACATTTTATTTCTTTTGGATAAA 240
 R hcv27464285 rpt
 | SNPG205 AL67188

.....
 Frame3 I R I C G I A G P C G N R W V T V * E T
 Frame2 T Y L W N C W A M W * * M G N C I R N C
 Frame1 Y V F V E L L G H V V I D G * L Y K K L
 DNA TACGTATTTGTGGAATTGCTGGGCCATGTGGTAATAGATGGGTAACGTATAAGAAACTG 300
 hcv26544778 Y rpt
 | SNPG298
 AL662833

.....
 Frame3 A I P L Y K L A A T F F A F L P A I S D
 Frame2 H T T L Q I G C H I F C I P T S N I R H
 Frame1 P Y H F T N W L P H F L H S Y Q Q Y Q T
 DNA CCATACCACTTTACAAATTGGCTGCCACATTTTTTGCATTCTACCAGCAATATCAGACA 360
 hcv27464284 K rpt
 | SNPG354

AL67188

Y hcv27465835 rpt
 | SNPG333 AL67188

.....
 Frame3 I P I F S I F L P V L R L I I C L F N F
 Frame2 S Y F F H I L A S V K T Y H M S F * L Y
 Frame1 F L F F P Y S C Q C * D L S Y V F L T L
 DNA TTCCTATTTTCCATATTCTTGCCAGTGTTAAGACTTATCATATGTCTTTTAACTTTA 420

.....
 Frame3 I C S R * C V M V S H C G F N L H F F D
 Frame2 L L * V M C D G F S L W F * L A L L * *
 Frame1 S A L G D V * W F L I V V L T C T S L M
 DNA TCTGCTCTAGGTGATGTGTGATGGTTTCTCATTGTGGTTTAACTTGCATTCTTTGATG 480
 Y hcv27466112 rpt
 | SNPG421 AL67188

| W SNPG476
 AL67188

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FIGURE 1B

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Frame3 D * Y C L L S F H V H L S D L L H I F Y
Frame2 L V L F A I F S C S S K R L I T Y I L *
Frame1 T S I V C Y L F M F I * A T Y Y I Y F M
DNA ACTAGTATTGTTTGCTATCTTTTCATGTTTCATCTAAGCGACTTATTACATATATTTTATG 540
      hcv27465418 Y hcv27468076 Y
      | SNPG518 AL67188
      AL67188| SNPG539
.....
Frame3 E L F C K F N D * F Q R L F Q N S L V F
Frame2 T I L Q I Q * L I P E T F S E F P S V F
Frame1 N Y F A N S M I N S R D F F R I P * C F
DNA AACTATTTTGCAAATTCAATGATTAATTCCAGAGACTTTTTCAGAAATTCCTAGTGTTTT 600
.....
Frame3 S T Y T M K L V T K K D F H F F L S Y P
Frame2 Y I Y N E V G D K E R L S F L P F L S I
Frame1 L H I Q * S W * Q R K T F I S S F L I H
DNA CTACATATACAATGAAGTTGGTGACAAAGAAAGACTTTTCATTTCTTCCTTTCTTATCCAT 660
      | Y SNPG618 hcv26544780AL662833 AL67188
.....
Frame3 L I F F L L K L L L F G R D E V S L I R
Frame2 D L F S F K I I I Y I W * R * G L T Y Q A
Frame1 * S F F F * N Y Y Y L V E M R S H L S G
DNA TGATCTTTTTTCTTTTAAAATTATTATTATTTGGTAGAGATGAGGTCTCACTTATCAGGC 720
      |SNPG686
      | SNPG667 hcv27463682
      | SNPG710
.....
Frame3 L V S N S * S Q V I L P P Q P P K M Q G
Frame2 G L K L L I S S D P P T S A S Q N A G I
Frame1 W S Q T P D L K * S S H L S L P K C R D
DNA TGGTCTCAAACCTCTGATCTCAAGTGATCCTCCACCTCAGCCTCCCAAATGCAGGGAT 780
.....
Frame3 L Q A * A T M P G P C C T G * D D C * V
Frame2 T G M S H H A W S L L H W L G * L L G V
Frame1 Y R H E P P C L V L V A L V R M T V R C
DNA TACAGGCATGAGCCACCATGCCTGGTCCTTGTGCACTGGTTAGGATGACTGTTAGGTGT 840
      | SNPG829
.....
Frame3 F K Q E * * E L T C L F T R N L N K F T
Frame2 * T R M M R A H M F V Y K E L K Q I Y K
Frame1 L N K N D E S S H V C L Q G T * T N L Q
DNA TTAAACAAGAATGATGAGAGCTCACATGTTTGTGTTTACAAGGAACTTAAACAAATTTACAA 900
      LF1.1 ATGATGAGAGCTCACATGTTTGTGTTTACAA
      LF2.10 GCTCACATGTTTGTGTTTACAAGGAACTTAA
      | SNPG856
.....
Frame3 R K K P I P I K K W A K D I N R H F S E
Frame2 K K T H P H Q K V G K G Y K Q T L L R G
Frame1 E K N P S P S K S G Q R I * T D T S Q R
DNA GAAAAAACCCTATCCCCATCAAAAAGTGGGCAAAGGATATAAACAGACACTTCTCAGAGG 960
      | SNPG902 INS G DNA14AL1
      | SNPG908 INS A DNAP5AL1
      | SNPG930 Pan troglod. A
.....

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FIGURE 1C

Frame3 E D I Y V A K K H M K K S S H T Y M K R
Frame2 R H L R G Q E T Y E K K L T H V Y E T *
Frame1 K T F T W P R N I * K K A H T R I * N V begin
of homology orf1 to tre homologue <R154
DNA AAGACATTTACGTGGCCAAGAAACATATGAAAAAAGCTCACACACGTATATGAAACGTG 1020
| SNP1006 | End1stexon
| SNP1018
| SNP972
| R SNP975

.....
Frame3 D C L * S Y P K K N * F Q A T A V L L P
Frame2 L F I I L S K K E L I S S N S S I T S I
Frame1 T V Y N P I Q K R T D F K Q Q Q Y Y F H
DNA ACTGTTTATAATCCTATCCAAAAAAGAACTGATTTCAAGCAACAGCAGTATTACTTCCAT 1080
| SNP1048
| SNP1056
| SNP1069
| SNP1073
| SNP1079

.....
Frame3 F N T W T C K H Q K S H W R N * T T L *
Frame2 Q Y L D L Q T S K K P L E K L N D S L K
Frame1 S I L G P A N I K K A T G E T E R L S E
DNA TCAATACTTGGACCTGCAAACATCAAAAAAGCCACTGGAGAACTGAACGACTCTCTGAA 1140
.....
Frame3 K P * T K I * R S * N L E K T * G K G Q
Frame2 A L N * D M K K L K S G K N L R K R T G
Frame1 S L K L R Y E E V E I W K K L E E K D R
DNA AGCCTTAACTAAGATATGAAGAAGTTGAAATCTGGAAAAAAGGACAGG 1200
R
hcv15819424 | SNP1199

| SNP1181
| SNP1154

.....
Frame3 A G G S T V A T T K K A G N R K R G W Q
Frame2 R G K H S G Y N K K G R K Q E E R M A A
Frame1 Q G E A Q W L Q Q K R Q E T G R E D G S
DNA CAGGGGAAGCACAGTGGCTACAACAAAAAGGCAGGAAACAGGAAGAGAGGATGGCAGC 1260
| SNP1236

.....
Frame3 H V G * R F F G D C I G F Q R Q N P K E
Frame2 C W L K V L W R L Y W I P K T K P K R A
Frame1 M L A K G S L E I V L D S K D K T Q K S
DNA ATGTTGGCTAAAGTTCTTTGGAGATTGTATTGGATTCCAAAGACAAAACCCAAAAGAGC 1320
| SNP1262
| R SNP1263
| SNP1274

SNPG1319

.....
Frame3 Q W * K E * K M * D Q R E R S N H S K G
Frame2 M V K R M K N V R P K R K E Q S Q Q R N
Frame1 N G E K N E K C E T K E K G A I T A K E
DNA AATGGTGAAGAATGAAAAATGTGAGACCAAGAGAAAGGAGCAATCACAGCAAAGGAA 1380
| R SNP1334
.....

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FIGURE 1D

Frame3 T I H N D D G * K H Q L D Y N G C S K N
 Frame2 Y T Q * * W I K T S A * L * W M L K E C
 Frame1 L Y T M M M D K N I S L I I M D A Q R M
 DNA CTATACACAATGATGATGGATAAAACATCAGCTTGATTATAATGGATGCTCAAAGAATG 1440

| SNP14 SNPG1426

hcv27504712

.....
 Frame3 A G L S G F L Y F T F S Q C S * K S H Q
 Frame2 R I I R I P V F Y I L S V F L K K P S V
 Frame1 Q D Y Q D S C I L H S L S V P E K A I S
 DNA CAGGATTATCAGGATTCCTGTATTTTACATTCTCTCAGTGTTCCTGAAAAAGCCATCAGT 1500
 K hcv11691030 | R SNPG1489

hcv16030281

| Y SNPG1466

| SNPG1444

| SNPG1487 SNP13
| SNPG1495 T

Pan trogl.

.....
 Frame3 S R S H C * L D * S T P P R * F Y R Y M
 Frame2 Q E S L L A G L K H T S Q M I L * I H G
 Frame1 P G V T A S W I E A H L P D D S I D T W
 DNA CCAGGAGTCACTGCTAGCTGGATTGAAGCACACCTCCCAGATGATTCTATAGATACATGG 1560
 | SNPG1518

| SNPG1505 hcv15819434

| Y SNPG1508

| SNPG1521

| SNPG1554

.....
 Frame3 E E E G E C G V Y G T S * L V * F C K R
 Frame2 R R G G M W S I W Y F L T G L V L Q K I
 Frame1 K K R G N V E Y M V L L D W F S S A K D
 DNA AAGAAGAGGGGGAATGTGGAGTATATGGTACTTCTTGACTGGTTTAGTTCTGCAAAAGAT 1620

| SNPG1612 C Pan trogl.

.....
 Frame3 F T D W N N T L A S E R C T F Q V G K *
 Frame2 Y R L E Q H S G I * K M H F S S G K V K
 Frame1 L Q I G T T L W H L K D A L F K W E S K
 DNA TTACAGATTGGAACAACACTCTGGCATCTGAAAGATGCACTTTTCAAGTGGGAAAGTAAA 1680

| SNPG1630 hcv15819435

| SNPG1680

| SNPG1638 hcv15819436

.....
 Frame3 N C P V Q W A L G L W F * R E A I K T G
 Frame2 L S C A M G L G P L V L E G G Y K N W F
 Frame1 T V L C N G P W A F G F R G R L * K L V
 DNA ACTGTCCTGTGCAATGGGCCTTGGGCTTTTGGTTTTAGAGGGAGGCTATAAAAACTGGTT 1740
 | SNPGDEL17070

| SNPG1687

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FIGURE 1E

Frame3 S F A I P S I Q Q M L R S L H P H N T R
 Frame2 L C Y S Q Y T T N A K V T P P P Q H Q N
 Frame1 P L L F P V Y N K C * G H S T P T T P E
 DNA CCTTTGCTATTCCAGTATACAACAAATGCTAAGTCACTCCACCCCAACACCAGAA 1800
 | SNPG1742

.....
 Frame3 M K S C L S H W I L L I P H W K N Q F L
 Frame2 E E L S I S L D F T Y P S L E E S I P S
 Frame1 * R V V Y L I G F Y L S L I G R I N S F
 DNA TGAAGAGTTGTCTATCTCATTGGATTTACTTATCCCTCATTGGAAGAATCAATTCCTTC 1860
 | SNPG1810 Y
 | SNPG1813

| SNPG1841

.....
 Frame3 L N L L P R C H L H L * K W M K T * N *
 Frame2 K P A A E M P P P P I K V D E D I E L I
 Frame1 * T C C R D A T S T Y K S G * R H R I D
 DNA TAAACCTGCTGCCGAGATGCCACCTCCACCTATAAAAGTGGATGAAGACATAGAATTGAT 1920
 | SNPG1890
 | SNPG1895 hcv16030290

| SNPG1874
 | SNPG1875

| SNPG1907
 | SNPG1909

.....
 Frame3 * V I K * V I M I K M R G Q D H * I Y Q
 Frame2 S D Q I S D N D Q N E R T G P L N I S I
 Frame1 K * S N K * * * S K * E D R T T E Y I N
 DNA AAGTGATCAAATAAGTGATAATGATCAAAATGAGAGGACAGGACCACTGAATATATCAAT 1980
 | SNPG1957

| SNPG1921
 | SNPG1922

| SNPG1959

| SNPG1976

.....
 Frame3 F Q L N Q L L L L N L M F H P S F S Q C
 Frame2 P V E S V A A S K S D V S P I I Q P V P
 Frame1 S S * I S C C F * I * C F T H H S A S A
 DNA TCCAGTTGAATCAGTTGCTGCTTCTAAATCTGATGTTTCACCCATCATTCAGCCAGTGCC 2040
 | SNPG1992
 | SNPG1993

.....
 Frame3 L A * R M F H R L I I L K N W Q S N C L
 Frame2 S I K N V P Q I D H T K K L A V K L P E
 Frame1 * H K E C S T D * S Y * K T G S Q I A *
 DNA TAGCATAAAGAATGTTCCACAGATTGATCATACTAAAAAAGTGGCAGTCAAATTGCCTGA 2100
 | SNPG2096

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FIGURE 1F

Frame3 K S I * S N L K V Q I M S N S L L R M K
 Frame2 E H I I K S E S T N H E Q Q S P Q N E K
 Frame1 R A Y N Q I * K Y K S * A T V S S E * K
 DNA AGAGCATATAATCAAATCTGAAAGTACAAATCATGAGCAACAGTCTCCTCAGAATGAAAA 2160
 | SNPG2135

|| SNPG2110 del AA P. trogl.

| EXON 3A IN P7N

.....
 Frame3 K L F L I V P P S Q * F P L Q L S C * Q
 Frame2 V I P D C S T K P V V S S P T L M L T D
 Frame1 S Y S * L F H Q A S S F L S N S H V N R
 DNA AGTTATTCTGATTGTTCCACCAAGCCAGTAGTTTCCTCTCCAACCTCATGTTAACAGA 2220
 | SNPG2180 hcv16030297
 | SNPG2192
 | SNPG2193 G Pan troglod.

.....
 Frame3 M K K R L I F M Q K L L F * W R K T N K
 Frame2 E E K A H I H A E T A L L M E K N K Q E
 Frame1 * R K G S Y S C R N C S S N G E K Q T R
 DNA TGAAGAAAAGGCTCATATTCATGCAGAACTGCTCTTAATGGAGAAAAACAAACAAGA 2280
 | SNPG2275

| SNPG2230

.....
 Frame3 K K N F R K D S K G N R K K L R R E E H
 Frame2 K E L Q E R Q Q G K Q K E frame shift of homology
 orf3
 Frame1 K R T S G K T A R E T E R N * G G K N T
 DNA AAAAGAACTTCAGGAAAGACAGCAAGGGAAACAGAAAGAACTGAGGAGGGAAGAACACG 2340
 | SNPG2314

.....
 Frame3 E Q K A K K K Q E A E E N E I T Q K Q Q
 Frame2 A K S Q K E T R S * R K * N Y T E A T K
 Frame1 S K K P K R N K K L K K M K L H R S N K
 DNA AGCAAAAAGCCAAAAAGAAACAAGAAGCTGAAGAAAATGAAATTACACAGAAGCAACAAA 2400
 | SNPG2370
 | SNPG2375

.....
 Frame3 K A K E E M E K K E R E Q A K K E D K E
 Frame2 S K R R N G E E R T * T G Q E R G * R N
 Frame1 K Q K K K W R R K N V N R P R K R I K K
 DNA AAGCAAAAAGAAGAAATGGAGAAGAAAGAACGTGAACAGGCCAAGAAAGAGGATAAAGAAA 2460
 | SNPG2449

hcv16030298

.....
 Frame3 I S A K K G K E I T R V K R Q S K S D H
 Frame2 L S K E G Q R N N K S K K T K * K * S *
 Frame1 S Q Q R R A K K * Q E * K D K V K V I M
 DNA TCTCAGCAAAGAAGGGCAAAGAAATAACAAGAGTAAAAAGACAAAGTAAAAGTGATCATG 2520

.....T.....

FIGURE 1G

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.....
Frame3  V Q K K S T R D V S H T S A T G D S G S
Frame2  T E K V N K R C V P Y I C D R G G F R F R
Frame1  Y R K S Q Q E M C P I H L R Q G I Q V Q
DNA     TACAGAAAAGTCAACAAGAGATGTGTCCCATACATCTGCGACAGGGGATTCAAGTTCAG 2640
      _____|SNPG2618 R
                  |SNPG2619 Y

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FIGURE 2

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SEQ ID NO:3 58 DFKQQQYYFHSILGPANIKKATGETERLSESLKLRVEEVEIWKKLEEKDRQGEAQWLQOK
SEQ ID NO:4 78 DFKQQQDYFHSILGPGNIKKAVEEAEERLSESLKLRVEEAEVRKKLEEKDRQEEAQRLQOK
*****

SEQ ID NO:3 118 RQETGREDGSM LAKGSLEIVLDSKDKTQKSNGEKNEKCETKEKGAITAKELYTMMDKNI
SEQ ID NO:4 138 RQETGREDGGT LAKGSLENVLDSKDKTQKSNGEKNEKCETKEKGAITAKELYTMTDKNI
*****

SEQ ID NO:3 178 SLIIMDAQRMQDYQDSCILHSLSVPEKAISPGVTASWIEAHL PDDSIDTWKKRGNVEYMV
SEQ ID NO:4 198 SLIIMDARRMQDYQDSCILHSLSVPEEAISPGVTASWIEAHL PDDSKDTWKKRGNVEYV
*****

SEQ ID NO:3 238 LLDWFSSAKDLQIGTTLWHLKDALFKWE-----KGGYKNWFLCYSQYTTNAKV
SEQ ID NO:4 258 LLDWFSSAKDLQIGTTLRSLKDALFKWESKTVLRNEPLVLEGGYENWLLCYPQYTTNAKV
*****

SEQ ID NO:3 286 TPPPQHONEELSISLDFTYPSLEESIPSKPAAEMPPPPPIKVDEDIELISDQISDNDQNER
SEQ ID NO:4 318 TPPPRRQNEEVSISLDFTYPSLEESIPSKPAAQTTPPASIEVDENIELISGQ-----NER
*****

SEQ ID NO:3 346 TGPLNISIPVESVAASKSDVSPPIIQPVPSIKNVPQIDHTKKLAVKLPEEHI IKSESTNHE
SEQ ID NO:4 372 MGPLNISTPVEPVAAASKSDVSPPIIQPVPSIKNVPQIDRTKKPAVKLPEEHR IKSESTNHE
*****

SEQ ID NO:3 406 QQSPQNEKVIPDCSTKPVVSSPTLMLTDEEKAH IHAETALLMEKNKQEKELQERQQKQK
SEQ ID NO:4 432 QQSPQSGKVIPDRSTKPVVFSPTLMLTDEEKARIHAETALLMEKNKQEKELRERQQEEQK
*****

SEQ ID NO:3 466 E
SEQ ID NO:4 492 E
*
```


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FIGURE 3

```
rhodanese      *->tagelkalles.apkliliDvRspefGeryeyegGHIpGAvNvplee
                ta+el+ ++ +++ +li++D+ + + y+ ++I ++ vp e
SEQ ID NO:3    164  TAKELYTMMMDkNISLIIMDAQRM-----QDYQDSCILHSLVPEK 204

rhodanese      eiealldrsgilpdieklhlldpeelaklfgelgsskdkrvivycrsgr
                +i+ +++s+i++ hl++d +++k+ g+ + + +s +
SEQ ID NO:3    205  AISPGVTASWIEA-----HLPDDSIDTWKKRGNVEY---MVLLDWFSSAK 246

rhodanese      dllrnrrsalaalllkklgypeVyiLkGGykeWlak<-*
                + + ++ ++lk + kGGyk+W+ +
SEQ ID NO:3    247  ----DLQIGTTLWHLKDAL---FKWEKGGYKNWFLC 275
```

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FIGURE 4

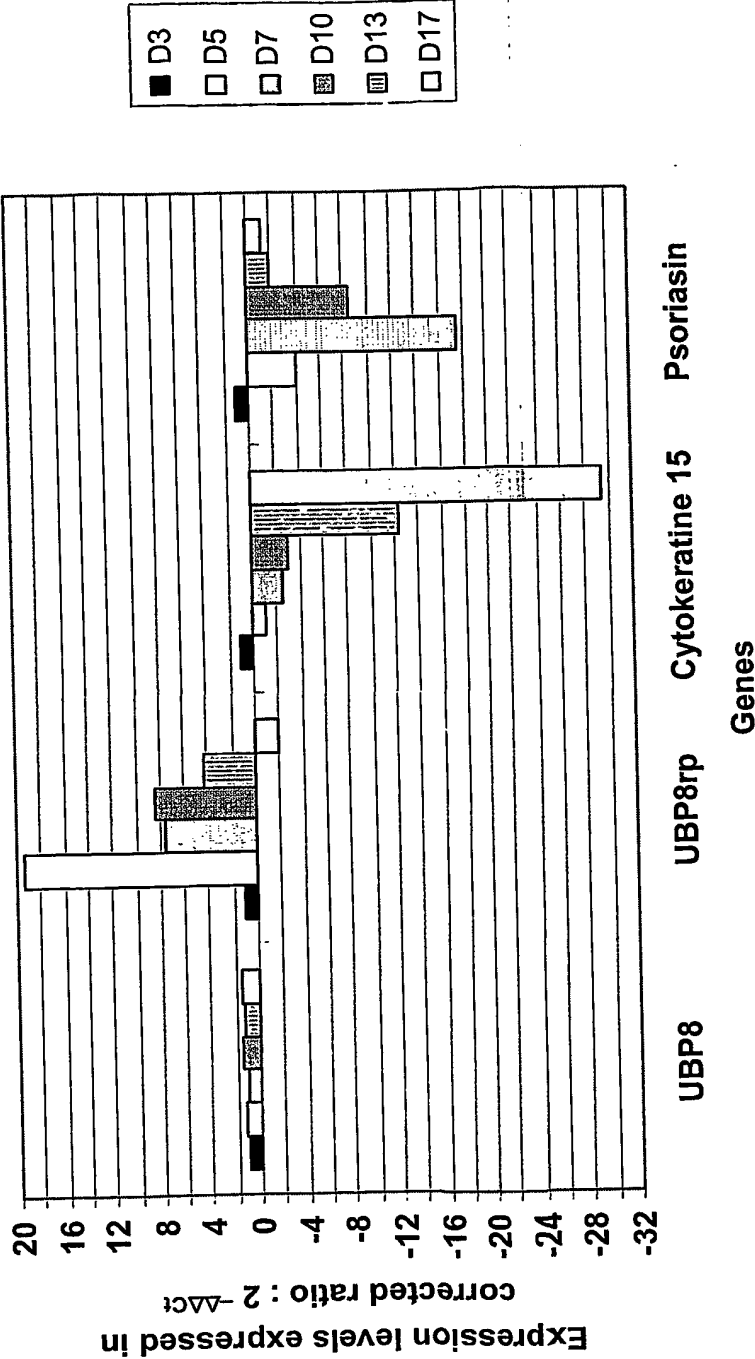
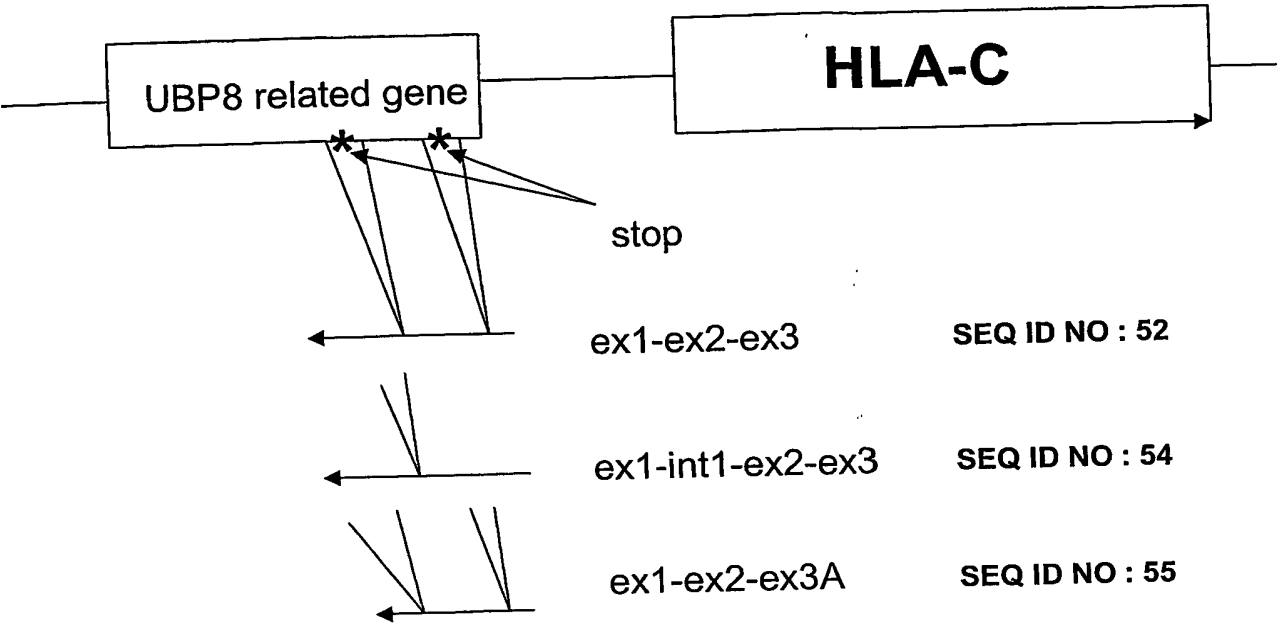


FIGURE 5



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FIGURE 6

```
SEQ ID NO:3      MMRAHMFVYKELKQIYKKKTHPHQKVGKGYKQTLRGRHLRGQETYEKKLTHVYETPDFK
SEQ ID NO:53     MMRAHMFVYKELKQIYKKKTHPHQKVGKGYKQTLRGRHLRGQETYEKKLTHVYETPDFK
SEQ ID NO:56     MMRAHMFVYKELKQIYKKKTHPHQKVGKGYKQTLRGRHLRGQETYEKKLTHVYETPDFK
                  *****

SEQ ID NO:3      QQQYFHSILGPANIKKATGETERLSESLKLYEEVEIWKKLEEKDRQGEAQLQKQKQE
SEQ ID NO:53     QQQDCFRSILGPANIKKATGETERLSESLKLYEEVEIWKKLEEKDRQGEAQLQKQKQE
SEQ ID NO:56     QQQDCFRSILGPANIKKATGETERLSESLKLYEEVEIWKKLEEKDRQGEAQLQKQKQE
                  *****

SEQ ID NO:3      TGREDSMLAKGSLEIVLDSKDKTQKSNGEKNKCEKKEGAIKAKELYTMMMDKNISLI
SEQ ID NO:53     TGREDSMLAKGSLEIVLDSKDKTQKSNGEKNKCEKKEGAIKAKELYTMMMDKNISLI
SEQ ID NO:56     TGREDSMLAKGSLEIVLDSKDKTQKSNGEKNKCEKKEGAIKAKELYTMMMDKNISLI
                  *****

SEQ ID NO:3      IMDAQRMQDYQDSCILHSLSVPEKAISPGVTASWIEAHLPPDSIDTWKRGNVYEMVLLD
SEQ ID NO:53     IMHAQRMQYYQDSCILHSLSVPEKAISPGVTASWIEAHLPPDSIDTWKRGNVYEMVLLD
SEQ ID NO:56     IMHAQRMQYYQDSCILHSLSVPEKAISPGVTASWIEAHLPPDSIDTWKRGNVYEMVLLD
                  *****

SEQ ID NO:3      WFSSAKDLQIGTTLWHLKDALFKWEKGGYKNWFLCYSQYTTNAKVTPPPQHNEELSISL
SEQ ID NO:53     WFSSAKDLQIGTTLWHLKDALFKWEKGGYKNWFFCYSQYTTNAKVTPPPQHNEELSISL
SEQ ID NO:56     WFSSAKDLQIGTTLWHLKDALFKWEK-----
                  *****

SEQ ID NO:3      DFTYPSLEESIPSKPAEMPPPIKVEDEIDELISDQISDNDQNERTGPLNISIPVESVAA
SEQ ID NO:53     DFTYPSLEESIPSKPAEMPPPIEVEDEIDELISDQISDNDQNERTGPLNISIPVESVAA
SEQ ID NO:56     -----

SEQ ID NO:3      SKSDVSPPIQPVPSIKNVPQIDHTKKLAVKLPEEHIIKSESTNHEQQSPQNEKVIPDCST
SEQ ID NO:53     SKSDVSPPIQPVPSIKNVPQIDHTKKLAVKLPEEHIIKSESTNHEQQSPQNEKVIPDCSA
SEQ ID NO:56     -----SPQNEKVIPDCSA
                  *****

SEQ ID NO:3      KPVVSSPTLMLTDEEKAHIIHAETALLMEKNKQEKELQERQQGKQKETEEGRTRAKSQKET
SEQ ID NO:53     KPVVSSPTLMLTDEEKAHIIHAETALLMEKNKQEKELQERQQGKQKETEEGRTRAKSQKET
SEQ ID NO:56     KPVVSSPTLMLTDEEKAHIIHAETALLMEKNKQEKELQERQQGKQKETEEGRTRAKSQKET
                  *****

SEQ ID NO:3      RS---
SEQ ID NO:53     RSCRK
SEQ ID NO:56     RSCRK
                  **
```